March 12, 2002

Via DHL

U.S. Patent and Trademark Office
Crystal Mall I
Seventh Floor, Receptionist
Attn: Examiner William Moore, Art Unit 1652
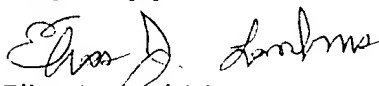1911 South Clark Street
Arlington, VA 22202

Re: U.S. Application No. 09/652,743 filed August 31, 2000
       "Proteases and Variants Thereof"

Dear Examiner Moore:

As per your request, enclosed is a computer readable form of the Sequence Listing mailed on October 22, 2001. The content of the paper copy that was filed on October 22, 2001 and of the enclosed computer readable form is the same. This submission contains no new matter.

If you have any questions, please do not hesitate to contact me.

Very truly yours,

Elias J. Lambiris
Director, Patents – US

W. Moore

1600 RUSH

Serial Number: 09/652,743A   ENTERED

CRF Processing Date: 3/13/2002
Edited by:
Verified by: _____ (STIC staff)

- [ ] Changed a file from non-ASCII to ASCII

- [ ] Changed the margins in cases where the sequence text was "wrapped" down to the next line.

- [ ] Edited a format error in the Current Application Data section, specifically: _____

- [ ] Edited the Current Application Data section with the actual current number. The number inputted by the applicant was [ ] the prior application data; or [ ] other _____.

- [ ] Added the mandatory heading and subheadings for "Current Application Data".

- [ ] Edited the "Number of Sequences" field. The applicant spelled out a number instead of using an integer.

- [ ] Changed the spelling of a mandatory field (the headings or subheadings), specifically: _____

- [ ] Corrected the SEQ ID NO when obviously incorrect. The sequence numbers that were edited were: _____

- [ ] Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited: _____

- [ ] Corrected subheading placement. All responses must be on the same line as each subheading. If the applicant placed a response below the subheading, this was moved to its appropriate place.

- [ ] Inserted colons after headings/subheadings. Headings edited included: _____

- [ ] Deleted extra, invalid, headings used by an applicant, specifically: _____

- [ ] Deleted: [ ] non-ASCII "garbage" at the beginning/end of files; [ ] secretary initials/filename at end of file; [ ] page numbers throughout text; [ ] other invalid text, such as _____.

- [ ] Inserted mandatory headings, specifically: _____

- [ ] Corrected an obvious error in the response, specifically: _____

- [ ] Edited identifiers where upper case is used but lower case is required, or vice versa.

- [ ] Corrected an error in the Number of Sequences field, specifically: _____

- [ ] A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted.

- [ ] Deleted *ending* stop codon in amino acid sequences and adjusted the "(A)Length:" field accordingly (error due to a PatentIn bug). Sequences corrected: _____

- [✓] Other: Corrected spelling of "Proteases" in C1207 response _____

*Examiner: Th abov corrections must be communicated to the applicant in th first Office Action. DO NOT send a copy of this form.

3/1/95

RAW SEQUENCE LISTING   DATE: 03/13/2002
PATENT APPLICATION: US/09/652,743A   TIME: 16:47:06

Input Set : A:\PTO.AMC.txt
Output Set: N:\CRF3\03132002\I652743A.raw

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        3 <110> APPLICANT: Norregaard-Madsen, Mads
        4        Ostergaard, Peter Rahbek
        5        Christensen, Claus Bo Voge
        6        Lassen, Soren Flensted
        8 <120> TITLE OF INVENTION: Novel Proteases And Variants Thereof
       10 <130> FILE REFERENCE: 5665.400-US
C-->   12 <140> CURRENT APPLICATION NUMBER: US/09/652,743A
C-->   12 <141> CURRENT FILING DATE: 2000-08-31
       12 <160> NUMBER OF SEQ ID NOS: 45
       14 <170> SOFTWARE: PatentIn version 3.1
       16 <210> SEQ ID NO: 1
       17 <211> LENGTH: 948
       18 <212> TYPE: DNA
       19 <213> ORGANISM: Bacillus
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       22 <221> NAME/KEY: CDS
       23 <222> LOCATION: (1)..(948)
       24 <223> OTHER INFORMATION:
       27 <220> FEATURE:
       28 <221> NAME/KEY: mat_peptide
       29 <222> LOCATION: (283)..()
       30 <223> OTHER INFORMATION:
       33 <220> FEATURE:
       34 <221> NAME/KEY: sig_peptide
       35 <222> LOCATION: (1)..(93)
       36 <223> OTHER INFORMATION:
       39 <220> FEATURE:
W-->   40 <221> NAME/KEY: pro-peptide
       41 <222> LOCATION: (94)..(282)
       42 <223> OTHER INFORMATION:
       45 <400> SEQUENCE: 1
       46 ttg gtt agt aaa aag agt gtt aaa cga ggt ttg atc aca ggt ctc att      48
       47 Leu Val Ser Lys Lys Ser Val Lys Arg Gly Leu Ile Thr Gly Leu Ile
       48             -90             -85             -80
       50 ggt att tct att tat tct tta ggt atg cac ccg gcc caa gcc gcg cca      96
       51 Gly Ile Ser Ile Tyr Ser Leu Gly Met His Pro Ala Gln Ala Ala Pro
       52             -75             -70             -65
       54 tcg cct cat act cct gtt tca agc gat cct tca tac aaa gcg gaa aca     144
       55 Ser Pro His Thr Pro Val Ser Ser Asp Pro Ser Tyr Lys Ala Glu Thr
       56          -60             -55             -50
       58 tcg gtt act tat gac cca cac att aag agc gat caa tac ggc ttg tat     192
       59 Ser Val Thr Tyr Asp Pro His Ile Lys Ser Asp Gln Tyr Gly Leu Tyr
       60       -45             -40             -35
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62 tca aaa gcg ttt aca ggc acc ggc aaa gtg aat gaa aca aag gaa aaa          240
63 Ser Lys Ala Phe Thr Gly Thr Gly Lys Val Asn Glu Thr Lys Glu Lys
64 -30               -25               -20               -15
66 gcg gaa aaa aag tca ccc gcc aaa gct cct tac agc att aaa tcg gtg          288
67 Ala Glu Lys Lys Ser Pro Ala Lys Ala Pro Tyr Ser Ile Lys Ser Val
68               -10               -5                -1  1
70 att ggt tct gat gat cgg aca agg gtc acc aac aca acc gca tat ccg          336
71 Ile Gly Ser Asp Asp Arg Thr Arg Val Thr Asn Thr Thr Ala Tyr Pro
72         5                 10                15
74 tac aga gcg atc gtt cat att tca agc agc atc ggt tca tgc acc gga          384
75 Tyr Arg Ala Ile Val His Ile Ser Ser Ser Ile Gly Ser Cys Thr Gly
76         20                25                30
78 tgg atg atc ggt ccg aaa acc gtc gca aca gcc gga cac tgc atc tat          432
79 Trp Met Ile Gly Pro Lys Thr Val Ala Thr Ala Gly His Cys Ile Tyr
80 35                40                45                50
82 gac aca tca agc ggt tca ttt gcc ggt aca gcc act gtt tcg ccg gga          480
83 Asp Thr Ser Ser Gly Ser Phe Ala Gly Thr Ala Thr Val Ser Pro Gly
84               55                60                65
86 cgg aac ggg aca agc tat cct tac ggc tca gtt aaa tcg acg cgc tac          528
87 Arg Asn Gly Thr Ser Tyr Pro Tyr Gly Ser Val Lys Ser Thr Arg Tyr
88               70                75                80
90 ttt att ccg tca gga tgg aga agc gga aac acc aat tac gat tac gga          576
91 Phe Ile Pro Ser Gly Trp Arg Ser Gly Asn Thr Asn Tyr Asp Tyr Gly
92         85                90                95
94 gca atc gaa cta agc gaa ccg atc ggc aat act gtc gga tac ttc gga          624
95 Ala Ile Glu Leu Ser Glu Pro Ile Gly Asn Thr Val Gly Tyr Phe Gly
96         100               105               110
98 tac tcg tac act act tca tca ctt gtt ggg aca act gtt acc atc agc          672
99 Tyr Ser Tyr Thr Thr Ser Ser Leu Val Gly Thr Thr Val Thr Ile Ser
100 115               120               125               130
102 ggc tac cca ggc gat aaa aca gca ggc aca caa tgg cag cat tca gga         720
103 Gly Tyr Pro Gly Asp Lys Thr Ala Gly Thr Gln Trp Gln His Ser Gly
104               135               140               145
106 ccg att gcc atc tcc gaa acg tat aaa ttg cag tac gca atg gac acg         768
107 Pro Ile Ala Ile Ser Glu Thr Tyr Lys Leu Gln Tyr Ala Met Asp Thr
108               150               155               160
110 tac gga gga caa agc ggt tca ccg gta ttc gaa caa agc agc tcc aga         816
111 Tyr Gly Gly Gln Ser Gly Ser Pro Val Phe Glu Gln Ser Ser Ser Arg
112         165               170               175
114 acg aac tgt agc ggt ccg tgc tcg ctt gcc gta cac aca aat gga gta         864
115 Thr Asn Cys Ser Gly Pro Cys Ser Leu Ala Val His Thr Asn Gly Val
116         180               185               190
118 tac ggc ggc tcc tcg tac aac aga ggc acc cgg att aca aaa gag gtg         912
119 Tyr Gly Gly Ser Ser Tyr Asn Arg Gly Thr Arg Ile Thr Lys Glu Val
120 195               200               205               210
122 ttc gac aat ttg acc aac tgg aaa aac agc gca caa                         948
123 Phe Asp Asn Leu Thr Asn Trp Lys Asn Ser Ala Gln
124               215               220
127 <210> SEQ ID NO: 2
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RAW SEQUENCE LISTING   DATE: 03/13/2002
PATENT APPLICATION: US/09/652,743A   TIME: 16:47:06

Input Set : A:\PTO.AMC.txt
Output Set: N:\CRF3\03132002\I652743A.raw

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129 <212> TYPE: PRT
130 <213> ORGANISM: Bacillus
132 <400> SEQUENCE: 2
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135               -90              -85              -80
138 Gly Ile Ser Ile Tyr Ser Leu Gly Met His Pro Ala Gln Ala Ala Pro
139           -75              -70              -65
142 Ser Pro His Thr Pro Val Ser Ser Asp Pro Ser Tyr Lys Ala Glu Thr
143           -60              -55              -50
146 Ser Val Thr Tyr Asp Pro His Ile Lys Ser Asp Gln Tyr Gly Leu Tyr
147       -45              -40              -35
150 Ser Lys Ala Phe Thr Gly Thr Gly Lys Val Asn Glu Thr Lys Glu Lys
151 -30              -25              -20              -15
154 Ala Glu Lys Lys Ser Pro Ala Lys Ala Pro Tyr Ser Ile Lys Ser Val
155           -10               -5              -1  1
158 Ile Gly Ser Asp Asp Arg Thr Arg Val Thr Asn Thr Thr Ala Tyr Pro
159       5                10               15
162 Tyr Arg Ala Ile Val His Ile Ser Ser Ser Ile Gly Ser Cys Thr Gly
163      20               25               30
166 Trp Met Ile Gly Pro Lys Thr Val Ala Thr Ala Gly His Cys Ile Tyr
167 35               40               45               50
170 Asp Thr Ser Ser Gly Ser Phe Ala Gly Thr Ala Thr Val Ser Pro Gly
171               55               60               65
174 Arg Asn Gly Thr Ser Tyr Pro Tyr Gly Ser Val Lys Ser Thr Arg Tyr
175           70               75               80
178 Phe Ile Pro Ser Gly Trp Arg Ser Gly Asn Thr Asn Tyr Asp Tyr Gly
179           85               90               95
182 Ala Ile Glu Leu Ser Glu Pro Ile Gly Asn Thr Val Gly Tyr Phe Gly
183       100              105              110
186 Tyr Ser Tyr Thr Thr Ser Ser Leu Val Gly Thr Thr Val Thr Ile Ser
187 115              120              125              130
190 Gly Tyr Pro Gly Asp Lys Thr Ala Gly Thr Gln Trp Gln His Ser Gly
191               135              140              145
194 Pro Ile Ala Ile Ser Glu Thr Tyr Lys Leu Gln Tyr Ala Met Asp Thr
195           150              155              160
198 Tyr Gly Gly Gln Ser Gly Ser Pro Val Phe Glu Gln Ser Ser Ser Arg
199           165              170              175
202 Thr Asn Cys Ser Gly Pro Cys Ser Leu Ala Val His Thr Asn Gly Val
203       180              185              190
206 Tyr Gly Gly Ser Ser Tyr Asn Arg Gly Thr Arg Ile Thr Lys Glu Val
207 195              200              205              210
210 Phe Asp Asn Leu Thr Asn Trp Lys Asn Ser Ala Gln
211           215              220
214 <210> SEQ ID NO: 3
215 <211> LENGTH: 1026
216 <212> TYPE: DNA
217 <213> ORGANISM: Bacillus
219 <220> FEATURE:
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RAW SEQUENCE LISTING   DATE: 03/13/2002
PATENT APPLICATION: US/09/652,743A   TIME: 16:47:06

Input Set : A:\PTO.AMC.txt
Output Set: N:\CRF3\03132002\I652743A.raw

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220 <221> NAME/KEY: CDS
221 <222> LOCATION: (1)..(1026)
222 <223> OTHER INFORMATION:
225 <220> FEATURE:
226 <221> NAME/KEY: mat_peptide
227 <222> LOCATION: (361)..()
228 <223> OTHER INFORMATION:
231 <220> FEATURE:
232 <221> NAME/KEY: sig_peptide
233 <222> LOCATION: (1)..(78)
234 <223> OTHER INFORMATION:
237 <220> FEATURE:
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W--> **238 <221> NAME/KEY: pro-peptide**
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239 <222> LOCATION: (79)..(360)
240 <223> OTHER INFORMATION:
243 <400> SEQUENCE: 3
244 atg  aaa cta cta tta aaa  ctt act ttt gta tgc  ata ttt atg tta      45
245 Met  Lys Leu Leu Leu Lys  Leu Thr Phe Val Cys  Ile Phe Met Leu
246 -120               -115               -110
248 agt  ggg att cta tcc cca  gta aac gca act caa  gct gag act ctt act  93
249 Ser  Gly Ile Leu Ser Pro  Val Asn Ala Thr Gln  Ala Glu Thr Leu Thr
250 -105               -100               -95                -90
252 aaa tta aat aaa ata agt  cag aag cag gaa cca  tca tat aaa cta gat  141
253 Lys Leu Asn Lys Ile Ser  Gln Lys Gln Glu Pro  Ser Tyr Lys Leu Asp
254                -85                -80                -75
256 gaa gaa atg gat tat gtt  cta att gat ttg gaa  aca caa tct gaa tcg  189
257 Glu Glu Met Asp Tyr Val  Leu Ile Asp Leu Glu  Thr Gln Ser Glu Ser
258                -70                -65                -60
260 att att tcg ata gga gat  aat acc gat ttg gga  gat caa tcg ttt act  237
261 Ile Ile Ser Ile Gly Asp  Asn Thr Asp Leu Gly  Asp Gln Ser Phe Thr
262        -55                -50                -45
264 tct tta ggg aag gtg gga  cat gga gaa ctt gag  aaa att aac tta gaa  285
265 Ser Leu Gly Lys Val Gly  His Gly Glu Leu Glu  Lys Ile Asn Leu Glu
266        -40                -35                -30
268 gaa ttt cgt aat cct aat  tta aca gta gta gac  ccg tta aca cgt aag  333
269 Glu Phe Arg Asn Pro Asn  Leu Thr Val Val Asp  Pro Leu Thr Arg Lys
270 -25                -20                -15                -10
272 cct att gaa caa aaa atc  agc cct ttt gtt gtt  ata ggc gat gat ggg  381
273 Pro Ile Glu Gln Lys Ile  Ser Pro Phe Val Val  Ile Gly Asp Asp Gly
274                -5                 -1 1               5
276 aga aga caa gtt caa aat  act tct ttc atg cca  ttt cgt gca ctt act  429
277 Arg Arg Gln Val Gln Asn  Thr Ser Phe Met Pro  Phe Arg Ala Leu Thr
278        10                 15                 20
280 tat att gag ttt gga aac  ctt aca agt aca tgg  agt tgt tct gga ggt  477
281 Tyr Ile Glu Phe Gly Asn  Leu Thr Ser Thr Trp  Ser Cys Ser Gly Gly
282        25                 30                 35
284 gtg att gga aca gat tta  gtt gtt act aat gca  cat tgt gta gaa ggt  525
285 Val Ile Gly Thr Asp Leu  Val Val Thr Asn Ala  His Cys Val Glu Gly
286 40                 45                 50                 55
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RAW SEQUENCE LISTING   DATE: 03/13/2002
PATENT APPLICATION: US/09/652,743A   TIME: 16:47:06

Input Set : **A:\PTO.AMC.txt**
Output Set: **N:\CRF3\03132002\I652743A.raw**

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288 tct gtg tta gca ggt act gta gtt cct ggt atg aac aat agt cag tgg        573
289 Ser Val Leu Ala Gly Thr Val Val Pro Gly Met Asn Asn Ser Gln Trp
290             60                  65                  70
292 gca tat ggg cat tat agg gtt act cag att atc tac cct gat caa tac        621
293 Ala Tyr Gly His Tyr Arg Val Thr Gln Ile Ile Tyr Pro Asp Gln Tyr
294             75                  80                  85
296 aga aat aac ggt gct tca gag ttt gat tat gct ata ctt aga gta gca        669
297 Arg Asn Asn Gly Ala Ser Glu Phe Asp Tyr Ala Ile Leu Arg Val Ala
298             90                  95                  100
300 cct gac tct gat gga cgt cat att gga aac aga gct gga att tta tct        717
301 Pro Asp Ser Asp Gly Arg His Ile Gly Asn Arg Ala Gly Ile Leu Ser
302        105                  110                  115
304 ttt aca gaa aca gga act gtt aac gaa aat act ttt cta aga acg tat        765
305 Phe Thr Glu Thr Gly Thr Val Asn Glu Asn Thr Phe Leu Arg Thr Tyr
306 120                  125                  130                  135
308 gga tac ccc ggt gat aaa ata tca gag aca aaa tta att tct ttg tgg        813
309 Gly Tyr Pro Gly Asp Lys Ile Ser Glu Thr Lys Leu Ile Ser Leu Trp
310                  140                  145                  150
312 gga atg gtt ggt cga tct gat gca ttt ttg cat cga gac cta ctg ttc        861
313 Gly Met Val Gly Arg Ser Asp Ala Phe Leu His Arg Asp Leu Leu Phe
314                  155                  160                  165
316 tac aat atg gac acc tat ttt ggt caa tca ggt tct cct gta tta aac        909
317 Tyr Asn Met Asp Thr Tyr Phe Gly Gln Ser Gly Ser Pro Val Leu Asn
318             170                  175                  180
320 agc gta gat tca atg gtt gcg gtt cat aat gca ggg tat atc gtt ggt        957
321 Ser Val Asp Ser Met Val Ala Val His Asn Ala Gly Tyr Ile Val Gly
322        185                  190                  195
324 ggt aat agg gaa att aat ggt ggt cct aaa atc aga aga gat ttt aca       1005
325 Gly Asn Arg Glu Ile Asn Gly Gly Pro Lys Ile Arg Arg Asp Phe Thr
326 200                  205                  210                  215
328 aac tta ttt aat caa atg aac                                          1026
329 Asn Leu Phe Asn Gln Met Asn
330                  220
333 <210> SEQ ID NO: 4
334 <211> LENGTH: 342
335 <212> TYPE: PRT
336 <213> ORGANISM: Bacillus
338 <400> SEQUENCE: 4
340 Met  Lys Leu Leu Leu Lys  Leu Thr Phe Val Cys  Ile Phe Met Leu
341 -120                -115                -110
344 Ser  Gly Ile Leu Ser Pro  Val Asn Ala Thr Gln Ala Glu Thr Leu Thr
345 -105                -100                -95                 -90
348 Lys Leu Asn Lys Ile Ser Gln Lys Gln Glu Pro Ser Tyr Lys Leu Asp
349             -85                 -80                 -75
352 Glu Glu Met Asp Tyr Val Leu Ile Asp Leu Glu Thr Gln Ser Glu Ser
353        -70                  -65                  -60
356 Ile Ile Ser Ile Gly Asp Asn Thr Asp Leu Gly Asp Gln Ser Phe Thr
357        -55                  -50                  -45
360 Ser Leu Gly Lys Val Gly His Gly Glu Leu Glu Lys Ile Asn Leu Glu
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RAW SEQUENCE LISTING ERROR SUMMARY   DATE: 03/13/2002
PATENT APPLICATION: US/09/652,743A   TIME: 16:47:07

Input Set : A:\PTO.AMC.txt
Output Set: N:\CRF3\03132002\I652743A.raw

Please Note:
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the
Sequence Listing to ensure that a corresponding explanation is presented in the <220>
to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:18; N Pos. 21,36
Seq#:20; N Pos. 12,15,18,21,24
Seq#:21; Xaa Pos. 2
Seq#:22; N Pos. 22,25,31
Seq#:23; Xaa Pos. 5
Seq#:24; N Pos. 15,18
Seq#:25; Xaa Pos. 6
Seq#:38; N Pos. 18,21,27
Seq#:39; Xaa Pos. 2,4
Seq#:40; N Pos. 12,15,21
Seq#:44; N Pos. 14,15

1600

RAW SEQUENCE LISTING   DATE: 03/13/2002
PATENT APPLICATION: US/09/652,743A   TIME: 16:16:04

Input Set : A:\sequence.ST25.txt
Output Set: N:\CRF3\03132002\I652743A.raw

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 3 <110> APPLICANT: Norregaard-Madsen, Mads
 4        Ostergaard, Peter Rahbek
 5        Christensen, Claus Bo Voge
 6        Lassen, Soren Flensted
 8 <120> TITLE OF INVENTION: Novel Proteases And Variants Thereof
10 <130> FILE REFERENCE: 5665.400-US
C--> 12 <140> CURRENT APPLICATION NUMBER: US/09/652,743A
C--> 12 <141> CURRENT FILING DATE: 2000-08-31
12 <160> NUMBER OF SEQ ID NOS: 45
14 <170> SOFTWARE: PatentIn version 3.1
16 <210> SEQ ID NO: 1
17 <211> LENGTH: 948
18 <212> TYPE: DNA
19 <213> ORGANISM: Bacillus
21 <220> FEATURE:
22 <221> NAME/KEY: CDS
23 <222> LOCATION: (1)..(948)
24 <223> OTHER INFORMATION:
27 <220> FEATURE:
28 <221> NAME/KEY: mat_peptide
29 <222> LOCATION: (283)..()
30 <223> OTHER INFORMATION:
33 <220> FEATURE:
34 <221> NAME/KEY: sig_peptide
35 <222> LOCATION: (1)..(93)
36 <223> OTHER INFORMATION:
39 <220> FEATURE:
W--> 40 <221> NAME/KEY: pro-peptide
41 <222> LOCATION: (94)..(282)
42 <223> OTHER INFORMATION:
45 <400> SEQUENCE: 1
46 ttg gtt agt aaa aag agt gtt aaa cga ggt ttg atc aca ggt ctc att      48
47 Leu Val Ser Lys Lys Ser Val Lys Arg Gly Leu Ile Thr Gly Leu Ile
48               -90               -85               -80
50 ggt att tct att tat tct tta ggt atg cac ccg gcc caa gcc gcg cca      96
51 Gly Ile Ser Ile Tyr Ser Leu Gly Met His Pro Ala Gln Ala Ala Pro
52               -75               -70               -65
54 tcg cct cat act cct gtt tca agc gat cct tca tac aaa gcg gaa aca     144
55 Ser Pro His Thr Pro Val Ser Ser Asp Pro Ser Tyr Lys Ala Glu Thr
56               -60               -55               -50
58 tcg gtt act tat gac cca cac att aag agc gat caa tac ggc ttg tat     192
59 Ser Val Thr Tyr Asp Pro His Ile Lys Ser Asp Gln Tyr Gly Leu Tyr
60       -45               -40               -35
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Input Set : A:\sequence.ST25.txt
Output Set: N:\CRF3\03132002\I652743A.raw

```
62  tca aaa gcg ttt aca ggc acc ggc aaa gtg aat gaa aca aag gaa aaa         240
63  Ser Lys Ala Phe Thr Gly Thr Gly Lys Val Asn Glu Thr Lys Glu Lys
64  -30              -25                  -20                  -15
66  gcg gaa aaa aag tca ccc gcc aaa gct cct tac agc att aaa tcg gtg         288
67  Ala Glu Lys Lys Ser Pro Ala Lys Ala Pro Tyr Ser Ile Lys Ser Val
68               -10                  -5                   -1  1
70  att ggt tct gat gat cgg aca agg gtc acc aac aca acc gca tat ccg         336
71  Ile Gly Ser Asp Asp Arg Thr Arg Val Thr Asn Thr Thr Ala Tyr Pro
72           5                   10                  15
74  tac aga gcg atc gtt cat att tca agc agc atc ggt tca tgc acc gga         384
75  Tyr Arg Ala Ile Val His Ile Ser Ser Ser Ile Gly Ser Cys Thr Gly
76      20                  25                  30
78  tgg atg atc ggt ccg aaa acc gtc gca aca gcc gga cac tgc atc tat         432
79  Trp Met Ile Gly Pro Lys Thr Val Ala Thr Ala Gly His Cys Ile Tyr
80  35                  40                  45                  50
82  gac aca tca agc ggt tca ttt gcc ggt aca gcc act gtt tcg ccg gga         480
83  Asp Thr Ser Ser Gly Ser Phe Ala Gly Thr Ala Thr Val Ser Pro Gly
84               55                  60                  65
86  cgg aac ggg aca agc tat cct tac ggc tca gtt aaa tcg acg cgc tac         528
87  Arg Asn Gly Thr Ser Tyr Pro Tyr Gly Ser Val Lys Ser Thr Arg Tyr
88               70                  75                  80
90  ttt att ccg tca gga tgg aga agc gga aac acc aat tac gat tac gga         576
91  Phe Ile Pro Ser Gly Trp Arg Ser Gly Asn Thr Asn Tyr Asp Tyr Gly
92           85                  90                  95
94  gca atc gaa cta agc gaa ccg atc ggc aat act gtc gga tac ttc gga         624
95  Ala Ile Glu Leu Ser Glu Pro Ile Gly Asn Thr Val Gly Tyr Phe Gly
96      100                 105                 110
98  tac tcg tac act act tca tca ctt gtt ggg aca act gtt acc atc agc         672
99  Tyr Ser Tyr Thr Thr Ser Ser Leu Val Gly Thr Thr Val Thr Ile Ser
100 115                 120                 125                 130
102 ggc tac cca ggc gat aaa aca gca ggc aca caa tgg cag cat tca gga        720
103 Gly Tyr Pro Gly Asp Lys Thr Ala Gly Thr Gln Trp Gln His Ser Gly
104                 135                 140                 145
106 ccg att gcc atc tcc gaa acg tat aaa ttg cag tac gca atg gac acg        768
107 Pro Ile Ala Ile Ser Glu Thr Tyr Lys Leu Gln Tyr Ala Met Asp Thr
108                 150                 155                 160
110 tac gga gga caa agc ggt tca ccg gta ttc gaa caa agc agc tcc aga        816
111 Tyr Gly Gly Gln Ser Gly Ser Pro Val Phe Glu Gln Ser Ser Ser Arg
112                 165                 170                 175
114 acg aac tgt agc ggt ccg tgc tcg ctt gcc gta cac aca aat gga gta        864
115 Thr Asn Cys Ser Gly Pro Cys Ser Leu Ala Val His Thr Asn Gly Val
116     180                 185                 190
118 tac ggc ggc tcc tcg tac aac aga ggc acc cgg att aca aaa gag gtg        912
119 Tyr Gly Gly Ser Ser Tyr Asn Arg Gly Thr Arg Ile Thr Lys Glu Val
120 195                 200                 205                 210
122 ttc gac aat ttg acc aac tgg aaa aac agc gca caa                        948
123 Phe Asp Asn Leu Thr Asn Trp Lys Asn Ser Ala Gln
124                 215                 220
127 <210> SEQ ID NO: 2
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RAW SEQUENCE LISTING   DATE: 03/13/2002
PATENT APPLICATION: US/09/652,743A   TIME: 16:16:04

Input Set : **A:\sequence.ST25.txt**
Output Set: **N:\CRF3\03132002\I652743A.raw**

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128 <211> LENGTH: 316
129 <212> TYPE: PRT
130 <213> ORGANISM: Bacillus
132 <400> SEQUENCE: 2
134 Leu Val Ser Lys Lys Ser Val Lys Arg Gly Leu Ile Thr Gly Leu Ile
135               -90                 -85                 -80
138 Gly Ile Ser Ile Tyr Ser Leu Gly Met His Pro Ala Gln Ala Ala Pro
139               -75                 -70                 -65
142 Ser Pro His Thr Pro Val Ser Ser Asp Pro Ser Tyr Lys Ala Glu Thr
143           -60                 -55                 -50
146 Ser Val Thr Tyr Asp Pro His Ile Lys Ser Asp Gln Tyr Gly Leu Tyr
147       -45                 -40                 -35
150 Ser Lys Ala Phe Thr Gly Thr Gly Lys Val Asn Glu Thr Lys Glu Lys
151 -30                 -25                 -20                 -15
154 Ala Glu Lys Lys Ser Pro Ala Lys Ala Pro Tyr Ser Ile Lys Ser Val
155               -10                 -5                  -1  1
158 Ile Gly Ser Asp Asp Arg Thr Arg Val Thr Asn Thr Thr Ala Tyr Pro
159           5                   10                  15
162 Tyr Arg Ala Ile Val His Ile Ser Ser Ser Ile Gly Ser Cys Thr Gly
163       20                  25                  30
166 Trp Met Ile Gly Pro Lys Thr Val Ala Thr Ala Gly His Cys Ile Tyr
167 35                  40                  45                  50
170 Asp Thr Ser Ser Gly Ser Phe Ala Gly Thr Ala Thr Val Ser Pro Gly
171               55                  60                  65
174 Arg Asn Gly Thr Ser Tyr Pro Tyr Gly Ser Val Lys Ser Thr Arg Tyr
175           70                  75                  80
178 Phe Ile Pro Ser Gly Trp Arg Ser Gly Asn Thr Asn Tyr Asp Tyr Gly
179       85                  90                  95
182 Ala Ile Glu Leu Ser Glu Pro Ile Gly Asn Thr Val Gly Tyr Phe Gly
183       100                 105                 110
186 Tyr Ser Tyr Thr Thr Ser Ser Leu Val Gly Thr Thr Val Thr Ile Ser
187 115                 120                 125                 130
190 Gly Tyr Pro Gly Asp Lys Thr Ala Gly Thr Gln Trp Gln His Ser Gly
191               135                 140                 145
194 Pro Ile Ala Ile Ser Glu Thr Tyr Lys Leu Gln Tyr Ala Met Asp Thr
195               150                 155                 160
198 Tyr Gly Gly Gln Ser Gly Ser Pro Val Phe Glu Gln Ser Ser Ser Arg
199           165                 170                 175
202 Thr Asn Cys Ser Gly Pro Cys Ser Leu Ala Val His Thr Asn Gly Val
203       180                 185                 190
206 Tyr Gly Gly Ser Ser Tyr Asn Arg Gly Thr Arg Ile Thr Lys Glu Val
207 195                 200                 205                 210
210 Phe Asp Asn Leu Thr Asn Trp Lys Asn Ser Ala Gln
211               215                 220
214 <210> SEQ ID NO: 3
215 <211> LENGTH: 1026
216 <212> TYPE: DNA
217 <213> ORGANISM: Bacillus
219 <220> FEATURE:
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     220 <221> NAME/KEY: CDS
     221 <222> LOCATION: (1)..(1026)
     222 <223> OTHER INFORMATION:
     225 <220> FEATURE:
     226 <221> NAME/KEY: mat_peptide
     227 <222> LOCATION: (361)..()
     228 <223> OTHER INFORMATION:
     231 <220> FEATURE:
     232 <221> NAME/KEY: sig_peptide
     233 <222> LOCATION: (1)..(78)
     234 <223> OTHER INFORMATION:
     237 <220> FEATURE:
W--> 238 <221> NAME/KEY: pro-peptide
     239 <222> LOCATION: (79)..(360)
     240 <223> OTHER INFORMATION:
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     244 atg  aaa cta cta tta aaa  ctt act ttt gta tgc  ata ttt atg tta        45
     245 Met  Lys Leu Leu Leu Lys  Leu Thr Phe Val Cys  Ile Phe Met Leu
     246 -120                -115                -110
     248 agt  ggg att cta tcc cca  gta aac gca act caa  gct gag act ctt act    93
     249 Ser  Gly Ile Leu Ser Pro  Val Asn Ala Thr Gln  Ala Glu Thr Leu Thr
     250 -105                -100                -95                 -90
     252 aaa tta aat aaa ata agt cag aag cag gaa cca tca tat aaa cta gat      141
     253 Lys Leu Asn Lys Ile Ser Gln Lys Gln Glu Pro Ser Tyr Lys Leu Asp
     254                -85                -80                -75
     256 gaa gaa atg gat tat gtt cta att gat ttg gaa aca caa tct gaa tcg      189
     257 Glu Glu Met Asp Tyr Val Leu Ile Asp Leu Glu Thr Gln Ser Glu Ser
     258                -70                -65                -60
     260 att att tcg ata gga gat aat acc gat ttg gga gat caa tcg ttt act      237
     261 Ile Ile Ser Ile Gly Asp Asn Thr Asp Leu Gly Asp Gln Ser Phe Thr
     262          -55                -50                -45
     264 tct tta ggg aag gtg gga cat gga gaa ctt gag aaa att aac tta gaa      285
     265 Ser Leu Gly Lys Val Gly His Gly Glu Leu Glu Lys Ile Asn Leu Glu
     266      -40                -35                -30
     268 gaa ttt cgt aat cct aat tta aca gta gta gac ccg tta aca cgt aag      333
     269 Glu Phe Arg Asn Pro Asn Leu Thr Val Val Asp Pro Leu Thr Arg Lys
     270 -25                -20                -15                -10
     272 cct att gaa caa aaa atc agc cct ttt gtt gtt ata ggc gat gat ggg      381
     273 Pro Ile Glu Gln Lys Ile Ser Pro Phe Val Val Ile Gly Asp Asp Gly
     274                -5                 -1  1                5
     276 aga aga caa gtt caa aat act tct ttc atg cca ttt cgt gca ctt act      429
     277 Arg Arg Gln Val Gln Asn Thr Ser Phe Met Pro Phe Arg Ala Leu Thr
     278          10                 15                 20
     280 tat att gag ttt gga aac ctt aca agt aca tgg agt tgt tct gga ggt      477
     281 Tyr Ile Glu Phe Gly Asn Leu Thr Ser Thr Trp Ser Cys Ser Gly Gly
     282      25                 30                 35
     284 gtg att gga aca gat tta gtt gtt act aat gca cat tgt gta gaa ggt      525
     285 Val Ile Gly Thr Asp Leu Val Val Thr Asn Ala His Cys Val Glu Gly
     286 40                 45                 50                 55
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RAW SEQUENCE LISTING   DATE: 03/13/2002
PATENT APPLICATION: US/09/652,743A   TIME: 16:16:04

Input Set : A:\sequence.ST25.txt
Output Set: N:\CRF3\03132002\I652743A.raw

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288 tct gtg tta gca ggt act gta gtt cct ggt atg aac aat agt cag tgg      573
289 Ser Val Leu Ala Gly Thr Val Val Pro Gly Met Asn Asn Ser Gln Trp
290             60              65              70
292 gca tat ggg cat tat agg gtt act cag att atc tac cct gat caa tac      621
293 Ala Tyr Gly His Tyr Arg Val Thr Gln Ile Ile Tyr Pro Asp Gln Tyr
294             75              80              85
296 aga aat aac ggt gct tca gag ttt gat tat gct ata ctt aga gta gca      669
297 Arg Asn Asn Gly Ala Ser Glu Phe Asp Tyr Ala Ile Leu Arg Val Ala
298         90              95              100
300 cct gac tct gat gga cgt cat att gga aac aga gct gga att tta tct      717
301 Pro Asp Ser Asp Gly Arg His Ile Gly Asn Arg Ala Gly Ile Leu Ser
302     105             110             115
304 ttt aca gaa aca gga act gtt aac gaa aat act ttt cta aga acg tat      765
305 Phe Thr Glu Thr Gly Thr Val Asn Glu Asn Thr Phe Leu Arg Thr Tyr
306 120             125             130             135
308 gga tac ccc ggt gat aaa ata tca gag aca aaa tta att tct ttg tgg      813
309 Gly Tyr Pro Gly Asp Lys Ile Ser Glu Thr Lys Leu Ile Ser Leu Trp
310             140             145             150
312 gga atg gtt ggt cga tct gat gca ttt ttg cat cga gac cta ctg ttc      861
313 Gly Met Val Gly Arg Ser Asp Ala Phe Leu His Arg Asp Leu Leu Phe
314             155             160             165
316 tac aat atg gac acc tat ttt ggt caa tca ggt tct cct gta tta aac      909
317 Tyr Asn Met Asp Thr Tyr Phe Gly Gln Ser Gly Ser Pro Val Leu Asn
318         170             175             180
320 agc gta gat tca atg gtt gcg gtt cat aat gca ggg tat atc gtt ggt      957
321 Ser Val Asp Ser Met Val Ala Val His Asn Ala Gly Tyr Ile Val Gly
322     185             190             195
324 ggt aat agg gaa att aat ggt ggt cct aaa atc aga aga gat ttt aca     1005
325 Gly Asn Arg Glu Ile Asn Gly Gly Pro Lys Ile Arg Arg Asp Phe Thr
326 200             205             210             215
328 aac tta ttt aat caa atg aac                                         1026
329 Asn Leu Phe Asn Gln Met Asn
330                 220
333 <210> SEQ ID NO: 4
334 <211> LENGTH: 342
335 <212> TYPE: PRT
336 <213> ORGANISM: Bacillus
338 <400> SEQUENCE: 4
340 Met  Lys Leu Leu Leu Lys  Leu Thr Phe Val Cys  Ile Phe Met Leu
341 -120              -115            -110
344 Ser  Gly Ile Leu Ser Pro  Val Asn Ala Thr Gln Ala Glu Thr Leu Thr
345 -105             -100            -95             -90
348 Lys Leu Asn Lys Ile Ser Gln Lys Gln Glu Pro Ser Tyr Lys Leu Asp
349             -85             -80             -75
352 Glu Glu Met Asp Tyr Val Leu Ile Asp Leu Glu Thr Gln Ser Glu Ser
353             -70             -65             -60
356 Ile Ile Ser Ile Gly Asp Asn Thr Asp Leu Gly Asp Gln Ser Phe Thr
357         -55             -50             -45
360 Ser Leu Gly Lys Val Gly His Gly Glu Leu Glu Lys Ile Asn Leu Glu
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VERIFICATION SUMMARY   DATE: 03/13/2002
PATENT APPLICATION: **US/09/652,743A**   TIME: 16:16:05

Input Set : **A:\sequence.ST25.txt**
Output Set: **N:\CRF3\03132002\I652743A.raw**

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L:12 M:270 C: Current Application Number differs, Replaced Current Application No
L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:40 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:1
L:238 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:3
L:452 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:5
L:650 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:7
L:840 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:9
L:1038 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:11
L:1222 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:13
L:1459 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:18
L:1515 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:20
L:1534 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21
L:1565 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22
L:1584 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23
L:1609 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:24
L:1628 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:25
L:1847 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:38
L:1872 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:39
L:1903 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:40
L:1965 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:44
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